SEQUENCE LISTING

<110> Mack, David
      Gish, Kurt C..
      Eos Biotechnology, Inc.

<120> Novel Methods of Diagnosing Breast Cancer,
      Compositions, and Methods of Screening for Breast
      Cancer Modulators

<130> 018501-009700US

<140> US 09/642,034
<141> 2000-08-18

<150> US 09/268,865
<151> 1999-03-15

<150> US 09/450,810
<151> 1999-11-29

<150> US 09/453,137
<151> 1999-12-02

<150> US 09/525,361
<151> 2000-03-15

<150> WO PCT/US00/06952
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<170> PatentIn Ver. 2.1

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<213> Artificial Sequence

<220>
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      base sequence in BCR4 not found in published human
      LIV-1

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<210> 3
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:sequence in
     BCR4 containing two additional t residues not
     found in published human LIV-1

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<210> 4
<211> 2268
<212> DNA
<213> Homo sapiens

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<223> open reading frame encoding human breast cancer
     protein BCR4

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<213> Homo sapiens

<220>
<223> human breast cancer protein BCR4

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Thr Glu Lys Ile Ser Pro Asn Trp Glu Ser Gly Ile Asn Val Asp Leu
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Ala Ile Ser Thr Arg Gln Tyr His Leu Gln Gln Leu Phe Tyr Arg Tyr
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Gly Glu Asn Asn Ser Leu Ser Val Glu Gly Phe Arg Lys Leu Leu Gln
 65                  70                  75                  80
Asn Ile Gly Ile Asp Lys Ile Lys Arg Ile His Ile His His Asp His
                 85                  90                  95
Asp His His Ser Asp His Glu His His Ser Asp His Glu Arg His Ser
             100                 105                 110
Asp His Glu His His Ser Asp His Glu His His Ser Asp His Asp His
         115                 120                 125
His Ser His His Asn His Ala Ala Ser Gly Lys Asn Lys Arg Lys Ala
     130                 135                 140
Leu Cys Pro Asp His Asp Ser Asp Ser Ser Gly Lys Asp Pro Arg Asn
145                 150                 155                 160
Ser Gln Gly Lys Gly Ala His Arg Pro Glu His Ala Ser Gly Arg Arg
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Asn Val Lys Asp Ser Val Ser Ala Ser Glu Val Thr Ser Thr Val Tyr
             180                 185                 190
Asn Thr Val Ser Glu Gly Thr His Phe Leu Glu Thr Ile Glu Thr Pro
         195                 200                 205
Arg Pro Gly Lys Leu Phe Pro Lys Asp Val Ser Ser Ser Thr Pro Pro
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Ser Val Thr Ser Lys Ser Arg Val Ser Arg Leu Ala Gly Arg Lys Thr
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Asn Glu Ser Val Ser Glu Pro Arg Lys Gly Phe Met Tyr Ser Arg Asn
                 245                 250                 255
Thr Asn Glu Asn Pro Gln Glu Cys Phe Asn Ala Ser Lys Leu Leu Thr
             260                 265                 270
Ser His Gly Met Gly Ile Gln Val Pro Leu Asn Ala Thr Glu Phe Asn
         275                 280                 285
Tyr Leu Cys Pro Ala Ile Ile Asn Gln Ile Asp Ala Arg Ser Cys Leu
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Ile His Thr Ser Glu Lys Lys Ala Glu Ile Pro Pro Lys Thr Tyr Ser
305                 310                 315                 320
Leu Gln Ile Ala Trp Val Gly Gly Phe Ile Ala Ile Ser Ile Ile Ser
                 325                 330                 335
Phe Leu Ser Leu Leu Gly Val Ile Leu Val Pro Leu Met Asn Arg Val
             340                 345                 350
Phe Phe Lys Phe Leu Leu Ser Phe Leu Val Ala Leu Ala Val Gly Thr
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4

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Phe Met Phe Leu Val Glu His Val Leu Thr Leu Ile Lys Gln Phe Lys
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Asp Lys Lys Lys Lys Asn Gln Lys Lys Pro Glu Asn Asp Asp Asp Val
    450             455             460
Glu Ile Lys Lys Gln Leu Ser Lys Tyr Glu Ser Gln Leu Ser Thr Asn
465             470             475             480
Glu Glu Lys Val Asp Thr Asp Asp Arg Thr Glu Gly Tyr Leu Arg Ala
            485             490             495
Asp Ser Gln Glu Pro Ser His Phe Asp Ser Gln Gln Pro Ala Val Leu
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Glu Glu Glu Glu Val Met Ile Ala His Ala His Pro Gln Glu Val Tyr
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Asn Glu Tyr Val Pro Arg Gly Cys Lys Asn Lys Cys His Ser His Phe
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His Asp Thr Leu Gly Gln Ser Asp Asp Leu Ile His His His His Asp
545         ᷱ       550             555             560
Tyr His His Ile Leu His His His His His Gln Asn His His Pro His
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Ser His Ser Gln Arg Tyr Ser Arg Glu Glu Leu Lys Asp Ala Gly Val
            580             585             590
Ala Thr Leu Ala Trp Met Val Ile Met Gly Asp Gly Leu His Asn Phe
        595             600             605
Ser Asp Gly Leu Ala Ile Gly Ala Ala Phe Thr Glu Gly Leu Ser Ser
    610             615             620
Gly Leu Ser Thr Ser Val Ala Val Phe Cys His Glu Leu Pro His Glu
625             630             635             640
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Ala Val Leu Tyr Asn Ala Leu Ser Ala Met Leu Ala Tyr Leu Gly Met
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Ala Thr Gly Ile Phe Ile Gly His Tyr Ala Glu Asn Val Ser Met Trp
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Ile Phe Ala Leu Thr Ala Gly Leu Phe Met Tyr Val Ala Leu Val Asp
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Met Val Pro Glu Met Leu His Asn Asp Ala Ser Asp His Gly Cys Ser
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<220>
<223> Description of Artificial Sequence:amino acid
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      BCR4 cDNA
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<210> 7
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<212> PRT
<213> Artificial Sequence

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<223> Description of Artificial Sequence:cytokine
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      domain conserved motif

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<223> Xaa = any amino acid

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conclude